



CCG GAG CAC GCC GCC AGC GTG CCC ACC CAT TCA CCC TAC GCA CAG CCC Pro Glu His Ala Ala Ser Val Pro Thr His Ser Pro Tyr Ala Gln Pro 90 95 100	461
AGC TCC ACC TTC GAC ACC ATG TCG CCC GCG CCT GTC ATC CCC TCC AAC Ser Ser Thr Phe Asp Thr Met Ser Pro Ala Pro Val Ile Pro Ser Asn 105 110 115	509
ACC GAC TAT CCC GGA CCC CAC CAC TTC GAG GTC ACT TTC CAG CAG TCC Thr Asp Tyr Pro Gly Pro His His Phe Glu Val Thr Phe Gln Gln Ser 120 125 130	557
AGC ACG GCC AAG TCA GCC ACC TGG ACG TAC TCC CCA CTC TTG AAG AAA Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Pro Leu Leu Lys Lys 135 140 145 150	605
CTC TAC TGC CAG ATC GCC AAG ACA TGC CCC ATC CAG ATC AAG GTG TCC Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val Ser 155 160 165	653
GCC CCA CCG CCC CCG GCC ACC GCC ATC CGG GCC ATG CCT GTC TAC AAG Ala Pro Pro Pro Pro Gly Thr Ala Ile Arg Ala Met Pro Val Tyr Lys 170 175 180	701
AAG GCG GAG CAC GTG ACC GAC ATC GTG AAG CGC TGC CCC AAC CAC GAG Lys Ala Glu His Val Thr Asp Ile Val Lys Arg Cys Pro Asn His Glu 185 190 195	749
CTC GGG AGG GAC TTC AAC GAA GGA CAG TCT GCC CCA GCC AGC CAC CTC Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser Ala Pro Ala Ser His Leu 200 205 210	797
ATC CGT GTG GAA GGC AAT AAT CTC TCG CAG TAT GTG GAC GAC CCT GTC Ile Arg Val Glu Gly Asn Asn Leu Ser Gln Tyr Val Asp Asp Pro Val 215 220 225 230	845
ACC GGC AGG CAG AGC GTC GTG GTG CCC TAT GAG CCA CCA CAG GTG GGG Thr Gly Arg Gln Ser Val Val Val Pro Tyr Glu Pro Pro Gln Val Gly 235 240 245	893
ACA GAA TTC ACC ACC ATC CTG TAC AAC TTC ATG TGT AAC AGC AGC TGT Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys 250 255 260	941
GTG GGG GGC ATG AAC CGA CGG CCC ATC CTC ATC ATC ATC ACC CTG GAG Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Ile Thr Leu Glu 265 270 275	989
ACG CGG GAT GGG CAG GTG CTG GGC CGC CGG TCC TTC GAG GCC CGC ATC Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Ser Phe Glu Gly Arg Ile 280 285 290	1037
TGC GCC TGT CCT GGC CGC GAC CGA AAA GCC GAT GAG GAC CAC TAC CGG Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp His Tyr Arg 295 300 305 310	1085
GAG CAG CAG GCC TTG AAT GAG AGC TCC GCC AAG AAC GGG GCT GCC AGC Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala Lys Asn Gly Ala Ala Ser 315 320 325	1133
AAG CGC GCC TTC AAG CAG AGT CCC CCT GCC GTC CCC GCC CTG GGC CCG Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala Val Pro Ala Leu Gly Pro 330 335 340	1181
GGT GTG AAG AAG CGG CGG CAC GGA GAC GAG GAC ACG TAC TAC CTG CAG Gly Val Lys Lys Arg Arg His Gly Asp Glu Asp Thr Tyr Tyr Leu Gln 345 350 355	1229
GTG CGA GGC CGC GAG AAC TTC GAG ATC CTG ATG AAG CTG AAG GAG AGC Val Arg Gly Arg Glu Asn Phe Glu Ile Leu Met Lys Leu Lys Glu Ser 360 365 370	1277

CCG GAG CAC GCC GCC AGC GTG CCC ACC CAT TCA CCC TAC GCA CAG CCC  
Pro Glu His Ala Ala Ser Val Pro Thr His Ser Pro Tyr Ala Gln Pro  
90 95 100

Ans  
AS  
Cm

CTG GAG CTG ATG GAG TTG GTG CCG CAG CCG CTG GTA GAC TCC TAT CGG 1325  
 Leu Glu Leu Met Glu Leu Val Pro Gln Pro Leu Val Asp Ser Tyr Arg  
 375 380 385 390

CAG CAG CAG CAG CTC CTA CAG AGG CCG AGT CAC CTA CAG CCC CCA TCC 1373  
 Gln Gln Gln Gln Leu Leu Gln Arg Pro Ser His Leu Gln Pro Pro Ser  
 395 400 405

TAC GGG CCG CTC CTC TCG CCC ATG AAC AAG GTG CAC GGG GGC GTG AAC 1421  
 Tyr Gly Pro Val Leu Ser Pro Met Asn Lys Val His Gly Gly Val Asn  
 410 415 420

AAG CTG CCC TCC CTC AAC CAG CTG GTG GGC CAG CCT CCC CCG CAC AGC 1469  
 Lys Leu Pro Ser Val Asn Gln Leu Val Gly Gln Pro Pro Pro His Ser  
 425 430 435

TCG GCA GCT ACA CCC AAC CTG GGA CCT GTG GGC TCT GGG ATG CTC AAC 1517  
 Ser Ala Ala Thr Pro Asn Leu Gly Pro Val Gly Ser Gly Met Leu Asn  
 440 445 450

AAC CAC GGC CAC GCA GTG GCA GCC AAC AGC GAG ATG ACC AGC AGC CAC 1565  
 Asn His Gly His Ala Val Pro Ala Asn Ser Glu Met Thr Ser Ser His  
 455 460 465 470

GGC ACC CAG TCC ATG GTC TCG GGG TCC CAC TGC ACT CCG CCA CCC CCC 1613  
 Gly Thr Gln Ser Met Val Ser Gly Ser His Cys Thr Pro Pro Pro Pro  
 475 480 485

TAC CAC GCC GAC CCC AGC CTC GTC AAT TTT TTA ACA GGA TTG GGG TGT 1661  
 Tyr His Ala Asp Pro Ser Leu Val Ser Phe Leu Thr Gly Leu Gly Cys  
 490 495 500

CCA AAC TGC ATC GAG TAT TTC ACG TCC CAG GGG TTA CAG AGC ATT TAC 1709  
 Pro Asn Cys Ile Glu Tyr Phe Thr Ser Gln Gly Leu Gln Ser Ile Tyr  
 505 510 515

CAC CTG CAG AAC CTG ACC ATC GAG GAC CTG GGC GCC CTG AAG ATC CCC 1757  
 His Leu Gln Asn Leu Thr Ile Glu Asp Leu Gly Ala Leu Lys Ile Pro  
 520 525 530

GAG CAG TAT CGC ATG ACC ATC TGG CGG GGC CTG CAG GAC CTG AAG CAG 1805  
 Glu Gln Tyr Arg Met Thr Ile Trp Arg Gly Leu Gln Asp Leu Lys Gln  
 535 540 545 550

GGC CAC GAC TAC GGC GCC GCC GCG CAG CAG CTG CTC CGC TCC AGC AAC 1853  
 Gly His Asp Tyr Gly Ala Ala Ala Gln Gln Leu Leu Arg Ser Ser Asn  
 555 560 565

GCG GCC GCC ATT TCC ATC GGC GGC TCC GGG GAG CTG CAG CGC CAG CGG 1901  
 Ala Ala Ala Ile Ser Ile Gly Gly Ser Gly Glu Leu Gln Arg Gln Arg  
 570 575 580

GTC ATG GAG GCC GTG CAC TTC CGC GTG CGC CAC ACC ATC ACC ATC CCC 1949  
 Val Met Glu Ala Val His Phe Arg Val Arg His Thr Ile Thr Ile Pro  
 585 590 595

AAC CGC GGC GGC CCC GGC GCC GGC CCC GAC GAG TGG GCG GAC TTC GGC 1997  
 Asn Arg Gly Gly Pro Gly Ala Gly Pro Asp Glu Trp Ala Asp Phe Gly  
 600 605 610

TTC GAC CTG CCC GAC TGC AAG GCC CGC AAG CAG CCC ATC AAG GAG GAG 2045  
 Phe Asp Leu Pro Asp Cys Lys Ala Arg Lys Gln Pro Ile Lys Glu Glu  
 615 620 625 630

TTC ACG GAG GCC GAG ATC CAC TGAGGGGCGG GGCCAGCCA GAGCCTGTGC 2096  
 Phe Thr Glu Ala Glu Ile His  
 635

CACCGCCAG AGACCCAGGC CGCCTCGCTC TCCTTCCTGT GTCCAAACT GCCTCCGGAG 2156

GCAGGGCCTC CAGGCTGTGC CCGGGGAAAG GCAAGGTCCG GCCCATGCC CGGCACCTCA 2216

CCGGCCCCAG GAGAGGCCCA GCCACCAAAG CCGCCTGCGG ACAGCCTGAG TCACCTGCAG 2276  
AACCTTCTGG AGCTGCCCTA ATGCTGGGCT TCGGGGCGAG GGGCCGGCCC ACTCTCAGCC 2336  
CTGCCACTGC CGGGCGTGCT CCATGGCAGG CGTGGGTGGG GACCGCAGTG TCAGCTCCGA 2396  
CCTCCAGGCC TCATCCTAGA GACTCTGTCA TCTGCCGATC AAGCAAGGTC CTTCCAGAGG 2456  
AAAGATCCTT CTTGCTGGT GGACTGCCAA AAAGTATTTT GCGACATCTT TTGGTTCTGG 2516  
AGAGTGGTGA GCAGCCAAGC GACTGTGTCT GAAACACCGT GCATTTTCAG GGAATGTCCC 2576  
TAACGGGCTG GGGACTCTCT CTGCTGGACT TGGGAGTGGC CTTTGCCCCC AGCACACTGT 2636  
ATTCTGCGGG ACCGCCTCCT TCCTGCCCTT AACAACCACC AAAGTGTTCG TGAAATTGGA 2696  
GAAACTGGG GAAGGCGCAA CCCCTCCCAG GTGCGGGAAG CATCTGGTAC CGCCTCGGCC 2756  
AGTGCCCCCTC AGCCTGGCCA CAGTCACCTC TCCTTGGGGA ACCCTGGGCA GAAAGGGACA 2916  
GCCTGTCCTT AGAGGACCGG AAATTGTCAA TATTTGATAA AATGATACCC TTTTCTAC 2974

## (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ala Gln Ser Thr Thr Thr Ser Pro Asp Gly Gly Thr Thr Phe Glu  
1 5 10 15  
His Leu Trp Ser Ser Leu Glu Pro Asp Ser Thr Tyr Phe Asp Leu Pro  
20 25 30  
Gln Ser Ser Arg Gly Asn Asn Glu Val Val Gly Gly Thr Asp Ser Ser  
35 40 45  
Met Asp Val Phe His Leu Glu Gly Met Thr Thr Ser Val Met Ala Gln  
50 55 60  
Phe Asn Leu Leu Ser Ser Thr Met Asp Gln Met Ser Ser Arg Ala Ala  
65 70 75 80  
Ser Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His  
85 90 95  
Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala  
100 105 110  
Pro Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu  
115 120 125  
Val Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr  
130 135 140  
Ser Pro Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro  
145 150 155 160  
Ile Gln Ile Lys Val Ser Ala Pro Pro Pro Gly Thr Ala Ile Arg  
165 170 175  
Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Ile Val Lys  
180 185 190  
Arg Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln S r

mb  
AS  
Ct

195 200 205

Ala Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln  
210 215 220

Tyr Val Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr  
225 230 235 240

Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe  
245 250 255

Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu  
260 265 270

Ile Ile Ile Thr Leu Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg  
275 280 285

Ser Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala  
290 295 300

Asp Glu Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala  
305 310 315 320

Lys Asn Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala  
325 330 335

Val Pro Ala Leu Gly Pro Gly Val Lys Lys Arg Arg His Gly Asp Glu  
340 345 350

Asp Thr Tyr Tyr Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu  
355 360 365

Met Lys Leu Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro  
370 375 380

Leu Val Asp Ser Tyr Arg Gln Gln Gln Gln Leu Leu Gln Arg Pro Ser  
385 390 395 400

His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys  
405 410 415

Val His Gly Gly Val Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly  
420 425 430

Gln Pro Pro Pro His Ser Ser Ala Ala Thr Pro Asn Leu Gly Pro Val  
435 440 445

Gly Ser Gly Met Leu Asn Asn His Gly His Ala Val Pro Ala Asn Ser  
450 455 460

Glu Met Thr Ser Ser His Gly Thr Gln Ser Met Val Ser Gly Ser His  
465 470 475 480

Cys Thr Pro Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Ser Phe  
485 490 495

Leu Thr Gly Leu Gly Cys Pro Asn Cys Ile Glu Tyr Phe Thr Ser Gln  
500 505 510

Gly Leu Gln Ser Ile Tyr His Leu Gln Asn Leu Thr Ile Glu Asp Leu  
515 520 525

Gly Ala Leu Lys Ile Pro Glu Gln Tyr Arg Met Thr Ile Trp Arg Gly  
530 535 540

Leu Gln Asp Leu Lys Gln Gly His Asp Tyr Gly Ala Ala Ala Gln Gln  
545 550 555 560

Leu Leu Arg Ser Ser Asn Ala Ala Ala Ile Ser Ile Gly Gly Ser Gly  
565 570 575

Glu Leu Gln Arg Gln Arg Val Met Glu Ala Val His Phe Arg Val Arg

590

Gln Pro Ile Lys Glu Glu Phe Thr Glu Ala Glu Ile His  
625 630 635

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2034 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cebus apella*

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 156..1652

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

AGAGCGAGCT GCCCTCGGAG GCCGGTGTGA GGAAG ATG GCC CAG TCC ACC ACC 173  
Met Ala Gln Ser Thr Thr  
1 5

GAA CCA GAC AGC ACC TAC TTC GAC CTT CCC CAG TCA AGC CGG GGG AAT 269  
Glu Pro Asp Ser Thr Tyr Phe Asp Leu Pro Gln Ser Ser Arg Gly Asn  
25 30 35

GAG GGC ATG ACC ACA TCT GTC ATG GCC CAG TTC AAT TTG CTG AGC AGC 365  
Glu Gly Met Thr Thr Ser Val Met Ala Gln Phe Asn Leu Leu Ser Ser  
55 60 65 70

CCG GAG CAC GCC GCC AGC GTG CCC ACC CAT TCA CCC TAC GCA CAG CCC 461  
Pro Glu His Ala Ala Ser Val Pro Thr His Ser Pro Tyr Ala Gln Pro  
90 95 100

AGC TCC ACC TTC GAC ACC ATG TCG CCC GCG CCT GTC ATC CCC TCC AAC  
Ser Ser Thr Phe Asp Thr Met Ser Pro Ala Pro Val Ile Pro Ser Asn  
105 110 115

ACC GAC TAT CCC GGA CCC CAC CAC TTC GAG GTC ACT TTC CAG CAG TCC 557  
Thr Asp Tyr Pro Gly Pro His His Phe Glu Val Thr Phe Gln Gln Ser  
120 125 130

AGC ACG GCC AAG TCA GCC ACC TGG ACG TAC TCC CCA CTC TTG AAG AAA 605

all  
AS  
WA

(2) INFORMATION FOR SEQ ID NO: 4:

(A) LENGTH: 499 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met	Ala	Gln	Ser	Thr	Thr	Ser	Pro	Asp	Gly	Gly	Thr	Thr	Phe	Glu	
1				5				10					15		
His	Leu	Trp	Ser	Ser	Leu	Glu	Pro	Asp	Ser	Thr	Tyr	Phe	Asp	Leu	Pro
			20					25					30		
Gln	Ser	Ser	Arg	Gly	Asn	Asn	Glu	Val	Val	Gly	Gly	Thr	Asp	Ser	Ser
		35					40					45			
Met	Asp	Val	Phe	His	Leu	Glu	Gly	Met	Thr	Thr	Ser	Val	Met	Ala	Gln
	50					55					60				
Phe	Asn	Leu	Leu	Ser	Ser	Thr	Met	Asp	Gln	Met	Ser	Ser	Arg	Ala	Ala
65					70					75					80
Ser	Ala	Ser	Pro	Tyr	Thr	Pro	Glu	His	Ala	Ala	Ser	Val	Pro	Thr	His
				85					90					95	
Ser	Pro	Tyr	Ala	Gln	Pro	Ser	Ser	Thr	Phe	Asp	Thr	Met	Ser	Pro	Ala
			100					105					110		
Pro	Val	Ile	Pro	Ser	Asn	Thr	Asp	Tyr	Pro	Gly	Pro	His	His	Phe	Glu
		115					120					125			
Val	Thr	Phe	Gln	Gln	Ser	Ser	Thr	Ala	Lys	Ser	Ala	Thr	Trp	Thr	Tyr
	130					135					140				



Ser Pro Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro  
 145 150 155 160  
 Ile Gln Ile Lys Val Ser Ala Pro Pro Pro Gly Thr Ala Ile Arg  
 165 170 175  
 Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Ile Val Lys  
 180 185 190  
 Arg Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser  
 195 200 205  
 Ala Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln  
 210 215 220  
 Tyr Val Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr  
 225 230 235 240  
 Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe  
 245 250 255  
 Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu  
 260 265 270  
 Ile Ile Ile Thr Leu Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg  
 275 280 285  
 Ser Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala  
 290 295 300  
 Asp Glu Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala  
 305 310 315 320  
 Lys Asn Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala  
 325 330 335  
 Val Pro Ala Leu Gly Pro Gly Val Lys Lys Arg Arg His Gly Asp Glu  
 340 345 350  
 Asp Thr Tyr Tyr Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu  
 355 360 365  
 Met Lys Leu Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro  
 370 375 380  
 Leu Val Asp Ser Tyr Arg Gln Gln Gln Gln Leu Leu Gln Arg Pro Ser  
 385 390 395 400  
 His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys  
 405 410 415  
 Val His Gly Gly Val Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly  
 420 425 430  
 Gln Pro Pro Pro His Ser Ser Ala Ala Thr Pro Asn Leu Gly Pro Val  
 435 440 445  
 Gly Ser Gly Met Leu Asn Asn His Gly His Ala Val Pro Ala Asn Ser  
 450 455 460  
 Glu Met Thr Ser Ser His Gly Thr Gln Ser Met Val Ser Gly Ser His  
 465 470 475 480  
 Cys Thr Pro Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Arg Thr  
 485 490 495  
 Trp Gly Pro

(2) INFORMATION FOR SEQ ID NO: 5:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2156 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 33..1940

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GCGAGCTGCC CTCGAGGCC GCGGTGGGGA AG ATG GCC CAG TCC ACC GCC ACC 53  
 Met Ala Gln Ser Thr Ala Thr  
 1 5

TCC CCT GAT GGG GGC ACC ACG TTT GAG CAC CTC TGG AGC TCT CTG GAA 101  
 Ser Pro Asp Gly Gly Thr Thr Phe Glu His Leu Trp Ser Ser Leu Glu  
 10 15 20

CCA GAC AGC ACC TAC TTC GAC CTT CCC CAG TCA AGC CGG GGG AAT AAT 149  
 Pro Asp Ser Thr Tyr Phe Asp Leu Pro Gln Ser Ser Arg Gly Asn Asn  
 25 30 35

GAG GTG GTG GGC GGA ACG GAT TCC AGC ATG GAC GTC TTC CAC CTG GAG 197  
 Glu Val Val Gly Gly Thr Asp Ser Ser Met Asp Val Phe His Leu Glu  
 40 45 50 55

GGC ATG ACT ACA TCT GTC ATG GCC CAG TTC AAT CTG CTG AGC AGC ACC 245  
 Gly Met Thr Thr Ser Val Met Ala Gln Phe Asn Leu Leu Ser Ser Thr  
 60 65 70

ATG GAC CAG ATG AGC AGC CGC GCG GCC TCG GCC AGC CCC TAC ACC CCA 293  
 Met Asp Gln Met Ser Ser Arg Ala Ala Ser Ala Ser Pro Tyr Thr Pro  
 75 80 85

GAG CAC GCC GCC AGC GTG CCC ACC CAC TCG CCC TAC GCA CAA CCC AGC 341  
 Glu His Ala Ala Ser Val Pro Thr His Ser Pro Tyr Ala Gln Pro Ser  
 90 95 100

TCC ACC TTC GAC ACC ATG TCG CCG GCG CCT GTC ATC CCC TCC AAC ACC 389  
 Ser Thr Phe Asp Thr Met Ser Pro Ala Pro Val Ile Pro Ser Asn Thr  
 105 110 115

GAC TAC CCC GGA CCC CAC CAC TTT GAG GTC ACT TTC CAG CAG TCC AGC 437  
 Asp Tyr Pro Gly Pro His His Phe Glu Val Thr Phe Gln Gln Ser Ser  
 120 125 130 135

ACG GCC AAG TCA GCC ACC TGG ACG TAC TCC CCG CTC TTG AAG AAA CTC 485  
 Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Pro Leu Leu Lys Lys Leu  
 140 145 150

TAC TGC CAG ATC GCC AAG ACA TGC CCC ATC CAG ATC AAG GTG TCC ACC 533  
 Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val Ser Thr  
 155 160 165

CCG CCA CCC CCA GGC ACT GCC ATC CCG GCC ATG CCT GTT TAC AAG AAA 581  
 Pro Pro Pro Pro Gly Thr Ala Ile Arg Ala Met Pro Val Tyr Lys Lys  
 170 175 180

GCG GAG CAC GTG ACC GAC GTC GTG AAA CGC TGC CCC AAC CAC GAG CTC 629  
 Ala Glu His Val Thr Asp Val Val Lys Arg Cys Pro Asn His Glu Leu  
 185 190 195

GGG AGG GAC TTC AAC GAA GGA CAG TCT GCT CCA GCC AGC CAC CTC ATC 677  
 Gly Arg Asp Phe Asn Glu Gly Gln Ser Ala Pro Ala Ser His Leu Ile  
 200 205 210 215

CGC GTG GAA GGC AAT AAT CTC TCG CAG TAT GTG GAT GAC CCT GTC ACC Arg Val Glu Gly Asn Asn Leu Ser Gln Tyr Val Asp Asp Pro Val Thr 220 225 230	725
GGC AGG CAG AGC GTC GTG GTG CCC TAT GAG CCA CCA CAG GTG GGG ACG Gly Arg Gln Ser Val Val Val Pro Tyr Glu Pro Pro Gln Val Gly Thr 235 240 245	773
GAA TTC ACC ACC ATC CTG TAC AAC TTC ATG TGT AAC AGC AGC TGT GTA Glu Phe Thr Thr Ile Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val 250 255 260	821
GGG GGC ATG AAC CGG CGG CCC ATC CTC ATC ATC ATC ACC CTG GAG ATG Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Ile Thr Leu Glu Met 265 270 275	869
CGG GAT GGG CAG GTG CTG GGC CGC CGG TCC TTT GAG GGC CGC ATC TGC Arg Asp Gly Gln Val Leu Gly Arg Arg Ser Phe Glu Gly Arg Ile Cys 280 285 290 295	917
GCC TGT CCT GGC CGC GAC GGA AAA GCT GAT GAG GAC CAC TAC CGG GAG Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp His Tyr Arg Glu 300 305 310	965
CAG CAG GCC CTG AAC GAG AGC TCC GCC AAG AAC GGG GCC GCC AGC AAG Gln Gln Ala Leu Asn Glu Ser Ser Ala Lys Asn Gly Ala Ala Ser Lys 315 320 325	1013
CGT GCC TTC AAG CAG AGC CCC CCT GCC GTC CCC GCC CTT GGT GCC GGT Arg Ala Phe Lys Gln Ser Pro Pro Ala Val Pro Ala Leu Gly Ala Gly 330 335 340	1061
GTG AAG AAG CGG CGG CAT GGA GAC GAG GAG ACG TAC TAC CTT CAG GTG Val Lys Lys Arg Arg His Gly Asp Glu Asp Thr Tyr Tyr Leu Gln Val 345 350 355	1109
CGA GGC CGG GAG AAC TTT GAG ATC CTG ATG AAG CTG AAA GAG AGC CTG Arg Gly Arg Glu Asn Phe Glu Ile Leu Met Lys Leu Lys Glu Ser Leu 360 365 370 375	1157
GAG CTG ATG GAG TTG GTG CCG CAG CCA CTG GTG GAC TCC TAT CGG CAG Glu Leu Met Glu Leu Val Pro Gln Pro Leu Val Asp Ser Tyr Arg Gln 380 385 390	1205
CAG CAG CAG CTC CTA CAG AGG CCG AGT CAC CTA CAG CCC CCG TCC TAC Gln Gln Gln Leu Leu Gln Arg Pro Ser His Leu Gln Pro Pro Ser Tyr 395 400 405	1253
GGG CCG GTC CTC TCG CCC ATG AAC AAG GTG CAC GGG GGC ATG AAC AAG Gly Pro Val Leu Ser Pro Met Asn Lys Val His Gly Gly Met Asn Lys 410 415 420	1301
CTG CCC TCC GTC AAC CAG CTG GTG GGC CAG CCT CCC CCG CAC AGT TCG Leu Pro Ser Val Asn Gln Leu Val Gly Gln Pro Pro Pro His Ser Ser 425 430 435	1349
GCA GCT ACA CCC AAC CTG GGG CCC GTG GGC CCC GGG ATG CTC AAC AAC Ala Ala Thr Pro Asn Leu Gly Pro Val Gly Pro Gly Met Leu Asn Asn 440 445 450 455	1397
CAT GGC CAC GCA GTG CCA GCC AAC GGC GAG ATG AGC AGC AGC CAC AGC His Gly His Ala Val Pro Ala Asn Gly Glu Met Ser Ser Ser His Ser 460 465 470	1445
GCC CAG TCC ATG GTC TCG GGG TCC CAC TGC ACT CCG CCA CCC CCC TAC Ala Gln Ser Met Val Ser Gly Ser His Cys Thr Pro Pro Pro Pro Tyr 475 480 485	1493
CAC GCC GAC CCC AGC CTC GTC AGT TTT TTA ACA GGA TTG GGG TGT CCA His Ala Asp Pro Ser Leu Val Ser Phe Leu Thr Gly Leu Gly Cys Pro 490 495 500	1541

60000-30000-400

me  
PS

AAC TGC ATC GAG TAT TTC ACC TCC CAA GGG TTA CAG AGC ATT TAC CAC 1589  
 Asn Cys Ile Glu Tyr Phe Thr Ser Gln Gly Leu Gln Ser Ile Tyr His  
 505 510 515  
 CTG GAG AAC CTG ACC ATT GAG GAC CTG GGG GCC CTG AAG ATC CCC GAG 1637  
 Leu Gln Asn Leu Thr Ile Glu Asp Leu Gly Ala Leu Lys Ile Pro Glu  
 520 525 530 535  
 CAG TAC CGC ATG ACC ATC TGG CGG GGC CTG CAG GAC CTG AAG CAG GGC 1685  
 Gln Tyr Arg Met Thr Ile Trp Arg Gly Leu Gln Asp Leu Lys Gln Gly  
 540 545 550  
 CAC GAC TAC AGC ACC GCG CAG CAG CTG CTC CGC TCT AGC AAC GCG GCC 1733  
 His Asp Tyr Ser Thr Ala Gln Gln Leu Leu Arg Ser Ser Asn Ala Ala  
 555 560 565  
 ACC ATC TCC ATC GGC GGC TCA GGG GAA CTG CAG CGC CAG CGG GTC ATG 1781  
 Thr Ile Ser Ile Gly Gly Ser Gly Glu Leu Gln Arg Gln Arg Val Met  
 570 575 580  
 GAG GCC GTG CAC TTC CGC GTG CGC CAC ACC ATC ACC ATC CCC AAC CGC 1829  
 Glu Ala Val His Phe Arg Val Arg His Thr Ile Thr Ile Pro Asn Arg  
 585 590 595  
 GGC GGC CCA GGC GGC GGC CCT GAC GAG TGG GCG GAC TTC GGC TTC GAC 1877  
 Gly Gly Pro Gly Gly Gly Pro Asp Glu Trp Ala Asp Phe Gly Phe Asp  
 600 605 610 615  
 CTG CCC GAC TGC AAG GCC CGC AAG CAG CCC ATC AAG GAG GAG TTC ACG 1925  
 Leu Pro Asp Cys Lys Ala Arg Lys Gln Pro Ile Lys Glu Glu Phe Thr  
 620 625 630  
 GAG GCC GAG ATC CAC TGAGGGCCTC GCCTGCTGC AGCCTGCGCC ACCGCCGAGA 1980  
 Glu Ala Glu Ile His  
 635  
 GACCCAAGCT GCCTCCCTC TCCTCCTGT GTGTCCAAA CTGCCTCAGG AGGCAGGACC 2040  
 TTCGGGCTGT GCCCGGGGAA AGGCAAGGTC CGGCCCATCC CCAGGCACCT CACAGGCCCC 2100  
 AGGAAAGGCC CAGCCACCGA AGCCGCCTGT GGACAGCCTG ATCACCTGC AGAACC 2156

## (2) INFORMATION FOR SEQ ID NO: 6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Ala Gln Ser Thr Ala Thr Ser Pro Asp Gly Gly Thr Thr Phe Glu  
 1 5 10 15  
 His Leu Trp Ser Ser Leu Glu Pro Asp Ser Thr Tyr Phe Asp Leu Pro  
 20 25 30  
 Gln Ser Ser Arg Gly Asn Asn Glu Val Val Gly Gly Thr Asp Ser Ser  
 35 40 45  
 Met Asp Val Phe His Leu Glu Gly Met Thr Thr Ser Val Met Ala Gln  
 50 55 60  
 Phe Asn Leu Leu Ser Ser Thr Met Asp Gln Met Ser Ser Arg Ala Ala  
 65 70 75 80  
 Ser Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His  
 85 90 95

mb  
AS

and  
ALX

```
(i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 2040 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
      (A) ORGANISM: Mus musculus

(ix) FEATURE:
      (A) NAME/KEY: CDS
      (B) LOCATION: 124..1890
```

GTGATCTCCCT	GTGGCCTGCA	GGGGACTGAG	CCAGGGAGTA	GATGCCCTGA	GACCCCAAGG	60
GACACCCAAG	GAAACCTTGC	TGGCTTTGAG	AAAGGGATCG	TCTCTCTCCT	GCCCAAGAGA	120
AGC ATG TGT ATG GGC CCT GTG TAT GAA TCC TTG GGG CAG GCC CAG TTC	Met Cys Met Gly Pro Val Tyr Glu Ser Leu Gly Gln Ala Gln Phe	168				
1	5	10	15			
AAT TTG CTC AGC AGT GCC ATG GAC CAG ATG GGC AGC CGT GCG GCC CCG	Asn Leu Leu Ser Ser Ala Met Asp Gln Met Gly Ser Arg Ala Ala Pro	216				
	20	25	30			
GCG AGC CCC TAC ACC CCG GAG CAC GCC GCC AGC GCG CCC ACC CAC TCG	Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Ala Pro Thr His Ser	264				
	35	40	45			
CCC TAC GCG CAG CCC AGC TCC ACC TTC GAC ACC ATG TCT CCG GCG CCT	Pro Tyr Ala Gln Pro Ser Ser Thr Ph Asp Thr M t Ser Pro Ala Pro	312				
	50	55	60			
GTC ATC CCT TCC AAT ACC GAC TAC CCC GGC CCC CAC CAC TTC GAG GTC						360

Val	Ile	Pro	Ser	Asn	Thr	Asp	Tyr	Pro	Gly	Pro	His	His	Phe	Glu	Val	
65							70									
ACC	TTC	CAG	CAG	TCG	AGC	ACT	GCC	AAG	TCG	GCC	ACC	TGG	ACA	TAC	TCC	408
Thr	Phe	Gln	Gln	Ser	Ser	Thr	Ala	Lys	Ser	Ala	Thr	Trp	Thr	Tyr	Ser	
90					85				90						95	
CCA	CTT	TTG	AAG	AAG	TTG	TAC	TGT	CAG	ATT	GCT	AAG	ACA	TGC	CCC	ATC	456
Pro	Leu	Leu	Lys	Lys	Leu	Tyr	Cys	Gln	Ile	Ala	Lys	Thr	Cys	Pro	Ile	
			100					105						110		
CAG	ATC	AAA	GTG	TCC	ACA	CCA	CCA	CCC	CCG	GGC	ACG	GCC	ATC	CGG	GCC	504
Gln	Ile	Lys	Val	Ser	Thr	Pro	Pro	Pro	Pro	Gly	Thr	Ala	Ile	Arg	Ala	
			115					120					125			
ATG	CCT	GTC	TAC	AAG	AAG	GCA	GAG	CAT	GTG	ACC	GAC	ATT	GTT	AAG	CGC	552
Met	Pro	Val	Tyr	Lys	Lys	Ala	Glu	His	Val	Thr	Asp	Ile	Val	Lys	Arg	
		130					135					140				
TGC	CCC	AAC	CAC	GAG	CTT	GGA	AGG	GAC	TTC	AAT	GAA	GGA	CAG	TCT	GCC	600
Cys	Pro	Asn	His	Glu	Leu	Gly	Arg	Asp	Phe	Asn	Glu	Gly	Gln	Ser	Ala	
	145					150					155					
CCG	GCT	AGC	CAC	CTC	ATC	CGT	GTA	GAA	GGC	AAC	AAC	CTC	GCC	CAG	TAC	648
Pro	Ala	Ser	His	Leu	Ile	Arg	Val	Glu	Gly	Asn	Asn	Leu	Ala	Gln	Tyr	
160					165				170						175	
GTG	GAT	GAC	CCT	GTC	ACC	GGA	AGG	CAG	AGT	GTG	GTT	GTG	CCG	TAT	GAA	696
Val	Asp	Asp	Pro	Val	Thr	Gly	Arg	Gln	Ser	Val	Val	Val	Pro	Tyr	Glu	
				180				185						190		
CCC	CCA	CAG	GTG	GGA	ACA	GAA	TTT	ACC	ACC	ATC	CTG	TAC	AAC	TTC	ATG	744
Pro	Pro	Gln	Val	Gly	Thr	Glu	Phe	Thr	Thr	Ile	Leu	Tyr	Asn	Phe	Met	
			195					200					205			
TGT	AAC	AGC	AGC	TGT	GTG	GGG	GGC	ATG	AAT	CGG	AGG	CCC	ATC	CTT	GTC	792
Cys	Asn	Ser	Ser	Cys	Val	Gly	Gly	Met	Asn	Arg	Arg	Pro	Ile	Leu	Val	
		210					215					220				
ATC	ATC	ACC	CTG	GAG	ACC	CGG	GAT	GGA	CAG	GTG	CTG	GGC	CGC	CGG	TCT	840
Ile	Ile	Thr	Leu	Glu	Thr	Arg	Asp	Gly	Gln	Val	Leu	Gly	Arg	Arg	Ser	
	225					230					235					
TTC	GAG	GGT	CGC	ATC	TGT	GCC	TGT	CCT	GGC	CGT	GAC	CGC	AAA	GCT	GAT	888
Phe	Glu	Gly	Arg	Ile	Cys	Ala	Cys	Pro	Gly	Arg	Asp	Arg	Lys	Ala	Asp	
240					245				250						255	
GAA	GAC	CAT	TAC	CGG	GAG	CAA	CAG	GCT	CTG	AAT	GAA	AGT	ACC	ACC	AAA	936
Glu	Asp	His	Tyr	Arg	Glu	Gln	Gln	Ala	Leu	Asn	Glu	Ser	Thr	Thr	Lys	
				260				265					270			
AAT	GGA	GCT	GCC	AGC	AAA	CGT	GCA	TTC	AAG	CAG	AGC	CCC	CCT	GCC	ATC	984
Asn	Gly	Ala	Ala	Ser	Lys	Arg	Ala	Phe	Lys	Gln	Ser	Pro	Pro	Ala	Ile	
			275					280					285			
CCT	GCC	CTG	GGT	ACC	AAC	GTG	AAG	AAG	AGA	CGC	CAC	GGG	GAC	GAG	GAC	1032
Pro	Ala	Leu	Gly	Thr	Asn	Val	Lys	Lys	Arg	Arg	His	Gly	Asp	Glu	Asp	
		290					295					300				
ATG	TTC	TAC	ATG	CAC	GTG	CGA	GGC	CGG	GAG	AAC	TTT	GAG	ATC	TTG	ATG	1080
Met	Phe	Tyr	Met	His	Val	Arg	Gly	Arg	Glu	Asn	Phe	Glu	Ile	Leu	Met	
		305				310					315					
AAA	GTC	AAG	GAG	AGC	CTA	GAA	CTG	ATG	GAG	CTT	GTG	CCC	CAG	CCT	TTG	1128
Lys	Val	Lys	Glu	Ser	Leu	Glu	Leu	Met	Glu	L	u	Val	Pro	Gln	Pro	
320					325				330						335	
GTT	GAC	TCC	TAT	CGA	CAG	CAG	CAG	CAG	CAG	CAG	CTC	CTA	CAG	AGG	CCG	1176
Val	Asp	Ser	Tyr	Arg	Gln	Gln	Gln	Gln	Gln	Gln	Leu	Leu	Gln	Arg	Pro	
				340				345						350		
AGT	CAC	CTG	CAG	CCT	CCA	TCC	TAT	GGG	CCC	GTG	CTC	TCC	CCA	ATG	AAC	1224

Ser His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn  
 355 360 365

AAG GTA CAC GGT GGT GTC AAC AAA CTG CCC TCC GTC AAC CAG CTG GTG 1272  
 Lys Val His Gly Gly Val Asn Lys Leu Pro Ser Val Asn Gln Leu Val  
 370 375 380

GGC CAG CCT CCC CCG CAC AGC TCA GCA GCT GGG CCC AAC CTG GGG CCC 1320  
 Gly Gln Pro Pro Pro His Ser Ser Ala Ala Gly Pro Asn Leu Gly Pro  
 385 390 395

ATG GGC TCC GGG ATG CTC AAC AGC CAC GGC CAC AGC ATG CCG GCC AAT 1368  
 Met Gly Ser Gly Met Leu Asn Ser His Gly His Ser Met Pro Ala Asn  
 400 405 410 415

GGT GAG ATG AAT GGA GGC CAC AGC TCC CAG ACC ATG GTT TCG GGA TCC 1416  
 Gly Glu Met Asn Gly Gly His Ser Ser Gln Thr Met Val Ser Gly Ser  
 420 425 430

CAC TGC ACC CCG CCA CCC CCC TAT CAT GCA GAC CCC AGC CTC GTC AGT 1464  
 His Cys Thr Pro Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Ser  
 435 440 445

TTT TTG ACA GGG TTG GGC TGT CCA AAC TGC ATC GAG TGC TTC ACT TCC 1512  
 Phe Leu Thr Gly Leu Gly Cys Pro Asn Cys Ile Glu Cys Phe Thr Ser  
 450 455 460

CAA GGG TTG CAG AGC ATC TAC CAC CTG CAG AAC CTT ACC ATC GAG GAC 1560  
 Gln Gly Leu Gln Ser Ile Tyr His Leu Gln Asn Leu Thr Ile Glu Asp  
 465 470 475

CTT GGG GCT CTG AAG GTC CCT GAC CAG TAC CGT ATG ACC ATC TGG AGG 1608  
 Leu Gly Ala Leu Lys Val Pro Asp Gln Tyr Arg Met Thr Ile Trp Arg  
 480 485 490 495

GGC CTA CAG GAC CTG AAG CAG AGC CAT GAC TGC GGC CAG CAA CTG CTA 1656  
 Gly Leu Gln Asp Leu Lys Gln Ser His Asp Cys Gly Gln Gln Leu Leu  
 500 505 510

CGC TCC AGC AGC AAC GCG GCC ACC ATC TCC ATC GGC GGC TCT GGC GAG 1704  
 Arg Ser Ser Ser Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu  
 515 520 525

CTG CAG CGG CAG CGG GTC ATG GAA GCC GTG CAT TTC CGT GTG CGC CAC 1752  
 Leu Gln Arg Gln Arg Val Met Glu Ala Val His Phe Arg Val Arg His  
 530 535 540

ACC ATC ACA ATC CCC AAC CGT GGA GGC GCA GGT GCG GTG ACA GGT CCC 1800  
 Thr Ile Thr Ile Pro Asn Arg Gly Gly Ala Gly Ala Val Thr Gly Pro  
 545 550 555

GAC GAG TGG GCG GAC TTT GGC TTT GAC CTG CCT GAC TGC AAG TCC CGT 1848  
 Asp Glu Trp Ala Asp Phe Gly Phe Asp Leu Pro Asp Cys Lys Ser Arg  
 560 565 570 575

AAG CAG CCC ATC AAA GAG GAG TTC ACA GAG ACA GAG AGC CAC 1890  
 Lys Gln Pro Ile Lys Glu Glu Phe Thr Glu Thr Glu Ser His  
 580 585

TGAGGAACGT ACCTTCTTCT CCTGTCCTTC CTCTGTGAGA AACTGCTCTT GGAAGTGGGA 1950  
 CCTGTTGGCT GTGCCACAG AAACCAGCAA GGACCTTCTG CCGGATGCCA TTCCTGAAGG 2010  
 GAAGTCGCTC ATGAACCTAAC TCCCTCTTGG 2040

## (2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 589 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear



mb.  
AS

Met Cys Met Gly Pro Val Tyr Glu Ser Leu Gly Gln Ala Gln Phe Asn  
1 5 10 15  
Leu Leu Ser Ser Ala Met Asp Gln Met Gly Ser Arg Ala Ala Pro Ala  
20 25 30  
Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Ala Pro Thr His Ser Pro  
35 40 45  
Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala Pro Val  
50 55 60  
Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu Val Thr  
65 70 75 80  
Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Pro  
85 90 95  
Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln  
100 105 110  
Ile Lys Val Ser Thr Pro Pro Pro Gly Thr Ala Ile Arg Ala Met  
115 120 125  
Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Ile Val Lys Arg Cys  
130 135 140  
Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser Ala Pro  
145 150 155 160  
Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ala Gln Tyr Val  
165 170 175  
Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr Glu Pro  
180 185 190  
Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe Met Cys  
195 200 205  
Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Val Ile  
210 215 220  
Ile Thr Leu Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Ser Phe  
225 230 235 240  
Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu  
245 250 255  
Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Thr Thr Lys Asn  
260 265 270  
Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala Ile Pro  
275 280 285  
Ala Leu Gly Thr Asn Val Lys Lys Arg Arg His Gly Asp Glu Asp Met  
290 295 300  
Phe Tyr Met His Val Arg Gly Arg Glu Asn Phe Glu Ile Leu Met Lys  
305 310 315 320  
Val Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro Leu Val  
325 330 335  
Asp Ser Tyr Arg Gln Gln Gln Gln Gln Leu Leu Gln Arg Pro Ser  
340 345 350  
His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys

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Met Cys Met Gly Pro Val Tyr Glu Ser Leu Gly Gln Ala Gln Phe Asn  
1 5 10 15  
Leu Leu Ser Ser Ala Met Asp Gln Met Gly Ser Arg Ala Ala Pro Ala  
20 25 30  
Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Ala Pro Thr His Ser Pro  
35 40 45  
Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala Pro Val  
50 55 60  
Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu Val Thr  
65 70 75 80  
Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Pro  
85 90 95  
Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln  
100 105 110  
Ile Lys Val Ser Thr Pro Pro Pro Gly Thr Ala Ile Arg Ala Met  
115 120 125  
Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Ile Val Lys Arg Cys  
130 135 140  
Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser Ala Pro  
145 150 155 160  
Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ala Gln Tyr Val  
165 170 175  
Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr Glu Pro  
180 185 190  
Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe Met Cys  
195 200 205  
Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Val Ile  
210 215 220  
Ile Thr Leu Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Ser Phe  
225 230 235 240  
Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu  
245 250 255  
Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Thr Thr Lys Asn  
260 265 270  
Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala Ile Pro  
275 280 285  
Ala Leu Gly Thr Asn Val Lys Lys Arg Arg His Gly Asp Glu Asp Met  
290 295 300  
Phe Tyr Met His Val Arg Gly Arg Glu Asn Phe Glu Ile Leu Met Lys  
305 310 315 320  
Val Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro Leu Val  
325 330 335  
Asp Ser Tyr Arg Gln Gln Gln Gln Gln Gln Leu Leu Gln Arg Pro Ser  
340 345 350  
His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu S r Pro Met Asn Lys

355 360 365

Val His Gly Gly Val Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly  
370 375 380

Gln Pro Pro Pro His Ser Ser Ala Ala Gly Pro Asn Leu Gly Pro Met  
385 390 395 400

Gly Ser Gly Met Leu Asn Ser His Gly His Ser Met Pro Ala Asn Gly  
405 410 415

Glu Met Asn Gly Gly His Ser Ser Gln Thr Met Val Ser Gly Ser His  
420 425 430

Cys Thr Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Ser Phe  
435 440 445

Leu Thr Gly Leu Gly Cys Pro Asn Cys Ile Glu Cys Phe Thr Ser Gln  
450 455 460

Gly Leu Gln Ser Ile Tyr His Leu Gln Asn Leu Thr Ile Glu Asp Leu  
465 470 475 480

Gly Ala Leu Lys Val Pro Asp Gln Tyr Arg Met Thr Ile Trp Arg Gly  
485 490 495

Leu Gln Asp Leu Lys Gln Ser His Asp Cys Gly Gln Gln Leu Leu Arg  
500 505 510

Ser Ser Ser Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu Leu  
515 520 525

Gln Arg Gln Arg Val Met Glu Ala Val His Phe Arg Val Arg His Thr  
530 535 540

Ile Thr Ile Pro Asn Arg Gly Gly Ala Gly Ala Val Thr Gly Pro Asp  
545 550 555 560

Glu Trp Ala Asp Phe Gly Phe Asp Leu Pro Asp Cys Lys Ser Arg Lys  
565 570 575

Gln Pro Ile Lys Glu Glu Phe Thr Glu Thr Glu Ser His  
580 585

## (2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 758 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Mus musculus
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 389..757

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TGGTCCCGCT TCGACCAAGA CTCCGGCTAC CAGCTTGCGG GCCCCGCGGA GGAGGAGACC 60

CCGCTGGGGC TAGCTGGGCG ACGCGCGCCA AGCGGCGGCG GGAAGGAGGC GGGAGGAGCG 120

GGGCCCAGAGA CCCCAGACTCG GGCAGAGCCA GCTGGGGAGG CGGGGCGCGC GTGGGAGCCA 180

GGGGCCCCGGG TGGCCGGCCC TCCTCCGCCA CGGCTGAGTG CCCGCGCTGC CTTCCCGCCG 240

GTCCGCCAAG AAAGGCGCTA AGCCTGCGGC AGTCCCCTCG CCGCCGCCTC CCTGCTCCGC 300  
 ACCCTTATAA CCGCGGTCC CGCATCCAGG CGAGGAGGCA ACGCTGCAGC CCAGCCCTCG 360  
 CCGACGCCGA CGCCCGGCCG GGAGCAGA ATG AGC GGC AGC GTT GGG GAG ATG 412  
 Met Ser Gly Ser Val Gly Glu Met  
 1 5  
 GCC CAG ACC TCT TCT TCC TCC TCC TCC ACC TTC GAG CAC CTG TGG AGT 460  
 Ala Gln Thr Ser Ser Ser Ser Ser Ser Thr Phe Glu His Leu Trp Ser  
 10 15 20  
 TCT CTA GAG CCA GAC AGC ACC TAC TTT GAC CTC CCC CAG CCC AGC CAA 508  
 Ser Leu Glu Pro Asp Ser Thr Tyr Phe Asp Leu Pro Gln Pro Ser Gln  
 25 30 35 40  
 GGG ACT AGC GAG GCA TCA GGC AGC GAG GAG TCC AAC ATG GAT GTC TTC 556  
 Gly Thr Ser Glu Ala Ser Gly Ser Glu Glu Ser Asn Met Asp Val Phe  
 45 50 55  
 CAC CTG CAA GGC ATG GCC CAG TTC AAT TTG CTC AGC AGT GCC ATG GAC 604  
 His Leu Gln Gly Met Ala Gln Phe Asn Leu Leu Ser Ser Ala Met Asp  
 60 65 70  
 CAG ATG GGC AGC CGT GCG GCC CCG GCG AGC CCC TAC ACC CCG GAG CAC 652  
 Gln Met Gly Ser Arg Ala Ala Pro Ala Ser Pro Tyr Thr Pro Glu His  
 75 80 85  
 GCC GCC AGC GCG CCC ACC CAC TCG CCC TAC GCG CAG CCC AGC TCC ACC 700  
 Ala Ala Ser Ala Pro Thr His Ser Pro Tyr Ala Gln Pro Ser Ser Thr  
 90 95 100  
 TTC GAC ACC ATG TCT CCG GCG CCT CTC ATC CCT TCC AAT ACC GAC TAC 748  
 Phe Asp Thr Met Ser Pro Ala Pro Val Ile Pro Ser Asn Thr Asp Tyr  
 105 110 115 120  
 CCC GGC CCC C  
 Pro Gly Pro 758

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 123 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Ser Gly Ser Val Gly Glu Met Ala Gln Thr Ser Ser Ser Ser Ser  
 1 5 10 15  
 Ser Thr Phe Glu His Leu Trp Ser Ser Leu Glu Pro Asp Ser Thr Tyr  
 20 25 30  
 Phe Asp Leu Pro Gln Pro Ser Gln Gly Thr Ser Glu Ala Ser Gly Ser  
 35 40 45  
 Glu Glu Ser Asn Met Asp Val Phe His Leu Gln Gly Met Ala Gln Phe  
 50 55 60  
 Asn Leu Leu Ser Ser Ala Met Asp Gln Met Gly Ser Arg Ala Ala Pro  
 65 70 75 80  
 Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Ala Pro Thr His Ser  
 85 90 95  
 Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala Pro  
 100 105 110

Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro  
115 120

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 559 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CGACCTTCCC CAGTCAAGCC GGGGGAATAA TGAGGTGGTG GGC GGAACGG ATTCCAGCAT 60  
GGACGTCTTC CACCTGGAGG GCATGACTAC ATCTGTCATG CATCCTCGGC TCCTGCCTCA 120  
CTAGCTGCGG AGCCTCTCCC GTCGGTCCA CGCTGCCGGG CGGCCACGAC CGTGACCCTT 180  
CCCCTCGGGC CGCCAGATC CATCCTCGT CCCACGGGAC ACCAGTTCCC TGGCGTGTGC 240  
AGACCCCCCG GCGCCTACCA TGCTGTACGT CCGTGACCCC GCACGGCACC TCGCCACGGC 300  
CCAGTTCAAT CTGCTGAGCA GCACCATGA CCAGATGAGC AGCCGCGCGG CCTCGGCCAG 360  
CCCCTACACC CCAGAGCAGC CCGCCAGCGT GCCCACCCAC TCGCCCTACG CACAACCCAG 420  
CTCCACCTTC GACACCATGT CGCCGGCGCC TGTCATCCCC TCCAACACCG ACTACCCCGG 480  
ACCCACCCAC TTTGAGGTCA CTTTCCAGCA GTCCAGCAGC GCCAAGTCAG CCACCTGGAC 540  
GTACTCCCCG CTCTTGAAG 559

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1764 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

ATGCTGTACG TCGGTGACCC CGCACGGCAC CTCGCCACGG CCCAGTTCAA TCTGTGAGC 60  
AGCACCATGG ACCAGATGAG CAGCCGCGCG GCCTCGGCCA GCCCCTACAC CCCAGAGCAC 120  
GCGCCAGCG TGCCACCCA CTCGCCCTAC GCACAACCCA GCTCCACCTT CGACACCATG 180  
TCGCCGGCGC CTGTCATCCC CTCCAACACC GACTACCCCG GACCCACCA CTTTGAGGTC 240  
ACTTTCAGC AGTCCAGCAC GGCCAAGTCA GCCACCTGGA CGTACTCCCC GCTCTTGAAG 300  
AAACTCTACT GCCAGATCGC CAAGACATGC CCCATCCAGA TCAAGGTGTC CACCCCGCCA 360  
CCCCCAGGCA CTGCCATCCG GGCCATGCCT GTTTACAAGA AAGCGGAGCA CGTGACCGAC 420  
GTCGTGAAAC GCTGCCCCAA CCACGAGCTC GGGAGGGACT TCAACGAAGG ACAGTCTGCT 480

CCAGCCAGCC ACCTCATCCG CGTGAAGGC AATAATCTCT CGCAGTATGT GGATGACCCT 540  
 GTCACCGGCA GGCAGAGCGT CGTGGTGCC TATGAGCCAC CACAGGTGGG GACGGAATTC 600  
 ACCACCATCC TGTACAACTT CATGTGTAAC AGCAGCTGTG TAGGGGGCAT GAACCGGCGG 660  
 CCCATCCTCA TCATCATCAC CCTGGAGATG CGGGATGGG AGGTGCTGGG CCGCCGGTCC 720  
 TTTGAGGGCC GCATCTGCGC CTGTCCTGGC CGCGACCGAA AAGCTGATGA GGACCACTAC 780  
 CGGGAGCAGC AGCCCTGAA CGAGAGCTCC GCCAAGAACG GGGCCGCCAG CAAGCGTGCC 840  
 TTCAAGCAGA GCCCCTGTC CGTCCCCGCC CTTGGTGCCG GTGTGAAGAA GCGGCGGCAT 900  
 GGAGACGAGG ACACGTAATA CCTTCAGGTG CGAGGCCGGG AGAACTTTGA GATCCTGATG 960  
 AAGCTGAAAG AGAGCCTGGA GCTGATGGAG TTGGTGCCGC AGCCACTGGT GGAATCCTAT 1020  
 CGGCAGCAGC AGCAGCTCCT ACAGAGGCCG AGTCACCTAC AGCCCCCGTC CTACGGGCCG 1080  
 GTCCTCTCGC CCATGAACAA GGTGCACGGG GGCATGAACA AGCTGCCCTC CGTCAACCAG 1140  
 CTGGTGGGCC AGCCTCCCCC GCACAGTTCC GCAGCTACAC CCAACCTGGG GCGCGTGGGC 1200  
 CCGGGGATGC TCAACAACCA TGGCCAGCA GTGCCAGCCA ACGGCGAGAT GAGCAGCAGC 1260  
 CACAGCGCCC AGTCCATGGT CTCGGGGTCC CACTGCACTC CGCCACCCCC CTACCACGCC 1320  
 GACCCAGCC TCGTCAGTTT TTTAACAGGA TTGGGGTGTC CAACTGTCAT CGAGTATTTT 1380  
 ACCTCCCAAG GGTACAGAG CATTTACCAC CTCAGAACC TGACCATTGA GGACCTGGGG 1440  
 GCCCTGAAGA TCCCCGAGCA GTACCGCATG ACCACTGGC GGGGCCTGCA GGACCTGAAG 1500  
 CAGGGCCACG ACTACAGCAC CGCGCAGCAG CTGCTCGCT CTAGCAACGC GGCCACCATC 1560  
 TCCATCGGCG GCTCAGGGGA ACTGCAGCGC CAGCGGGTCA TGGAGGCCGT GCACTTCCGC 1620  
 GTGCGCCACA CCATCACCAT CCCCACCGC GCGGCGCCAG GCGGCGGCC TGACGAGTGG 1680  
 GCGGACTTCG GCTTCGACCT GCGGACTGC AAGGCCGCA AGGAGCCAT CAAGGAGGAG 1740  
 TTCACGGAGG CCGAGATCCA CTGA 1764

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 587 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Met Leu Tyr Val Gly Asp Pro Ala Arg His Leu Ala Thr Ala Gln Phe  
 1 5 10 15  
 Asn Leu Leu Ser Ser Thr Met Asp Gln Met Ser Ser Arg Ala Ala Ser  
 20 25 30  
 Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His Ser  
 35 40 45  
 Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala Pro  
 50 55 60  
 Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu Val  
 65 70 75 80

ASX

Leu Gln Ser Ile Tyr His Leu Gln Asn Leu Thr Ile Glu Asp Leu Gly  
 465 470 475 480  
 Ala Leu Lys Ile Pro Glu Gln Tyr Arg Met Thr Ile Trp Arg Gly Leu  
 485 490 495  
 Gln Asp Leu Lys Gln Gly His Asp Tyr Ser Thr Ala Gln Gln Leu Leu  
 500 505 510  
 Arg Ser Ser Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu Leu  
 515 520 525  
 Gln Arg Gln Arg Val Met Glu Ala Val His Phe Arg Val Arg His Thr  
 530 535 540  
 Ile Thr Ile Pro Asn Arg Gly Gly Pro Gly Gly Gly Pro Asp Glu Trp  
 545 550 555 560  
 Ala Asp Phe Gly Phe Asp Leu Pro Asp Cys Lys Ala Arg Lys Gln Pro  
 565 570 575  
 Ile Lys Glu Glu Phe Thr Glu Ala Glu Ile His  
 580 585

## (2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1521 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo. sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

ATGCTGTACG TCGGTGACCC CGCACGGCAC CTCGCCACGG CCCAGTTCAA TCTGCTGAGC 60  
 AGCACCATGG ACCAGATGAG CAGCCGCGCG GCCTCGGCCA GCCCCTACAC CCCAGAGCAC 120  
 GCCGCCAGCG TGCCCACCCA CTCGCCCTAC GCACAACCCA GCTCCACCTT CGACACCATG 180  
 TCGCCGGCGC CTGTCTATCC CTCCAACACC GACTACCCCG GACCCACCA CTTTGAGGTC 240  
 ACTTTCAGC AGTCCAGCAC GGCCAAGTCA GCCACCTGGA CGTACTCCCC GCTCTTGAAG 300  
 AAATCTACT GCCAGATCGC CAAGACATGC CCCATCCAGA TCAAGGTGTC CACCCCGCCA 360  
 CCCCCAGGCA CTGCCATCCG GGCCATGCCT GTTTACAAGA AAGCGGAGCA CGTGACCGAC 420  
 GTCGTGAAC GCTGCCCCAA CCACGAGCTC GGGAGGGACT TCAACGAAGG ACAGTCTCT 480  
 CCAGCCAGCC ACCTCATCCG CGTGGAAGGC AATAATCTCT CGCAGTATGT GGATGACCCT 540  
 GTCACCGGCA GGCAGAGCGT CGTGGTGCCC TATGAGCCAC CACAGGTGGG GACGGAATTC 600  
 ACCACCATCC TGTACAACTT CATGTGTAAC AGCAGCTGTG TAGGGGGCAT GAACCGCGCG 660  
 CCCATCCTCA TCATCATCAC CCTGGAGATG CGGGATGGGC AGGTGCTGGG CCGCCGGTCC 720  
 TTTGAGGGCC GCATCTGCGC CTGTCCTGGC CGCGACCGAA AAGCTGATGA GGACCACTAC 780  
 CGGGAGCAGC AGGCCCTGAA CGAGAGCTCC GCCAAGAACG GGGCCGCCAG CAAGCGTGCC 840  
 TTCAAGCAGA GCCCCCTGC CGTCCCCGCC CTTGGTGCCG GTGTGAAGAA GCGCGGCAT 900  
 GGAGACGAGG ACACGTACTA CCTTCAGGTG CGAGGCCGGG AGAACTTTGA GATCCTGATG 960





Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile  
 210 215 220  
 Ile Ile Thr Leu Glu Met Arg Asp Gly Gln Val Leu Gly Arg Arg Ser  
 225 230 235 240  
 Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp  
 245 250 255  
 Glu Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala Lys  
 260 265 270  
 Asn Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala Val  
 275 280 285  
 Pro Ala Leu Gly Ala Gly Val Lys Lys Arg Arg His Gly Asp Glu Asp  
 290 295 300  
 Thr Tyr Tyr Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu Met  
 305 310 315 320  
 Lys Leu Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro Leu  
 325 330 335  
 Val Asp Ser Tyr Arg Gln Gln Gln Gln Leu Leu Gln Arg Pro Pro Arg  
 340 345 350  
 Asp Ala Gln Gln Pro Trp Pro Arg Ser Ala Ser Gln Arg Arg Asp Glu  
 355 360 365  
 Gln Gln Pro Gln Arg Pro Val His Gly Leu Gly Val Pro Leu His Ser  
 370 375 380  
 Ala Thr Pro Leu Pro Arg Arg Pro Gln Pro Arg Gln Asp Leu Gly Ala  
 385 390 395 400  
 Leu Lys Ile Pro Glu Gln Tyr Arg Met Thr Ile Trp Arg Gly Leu Gln  
 405 410 415  
 Asp Leu Lys Gln Gly His Asp Tyr Ser Thr Ala Gln Gln Leu Leu Arg  
 420 425 430  
 Ser Ser Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu Leu Gln  
 435 440 445  
 Arg Gln Arg Val Met Glu Ala Val His Phe Arg Val Arg His Thr Ile  
 450 455 460  
 Thr Ile Pro Asn Arg Gly Gly Pro Gly Gly Gly Pro Asp Glu Trp Ala  
 465 470 475 480  
 Asp Phe Gly Phe Asp Leu Pro Asp Cys Lys Ala Arg Lys Gln Pro Ile  
 485 490 495  
 Lys Glu Glu Phe Thr Glu Ala Glu Ile His  
 500 505

## (2) INFORMATION FOR SEQ ID NO: 16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1870 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (ix) FEATURE:

- (A) NAME/KEY: CDS

Paul  
AS  
W

TGCCCGGGG	TGCGACGGCT	GCAGGGAACC	AGACAGCACC	TACTTCGACC	TTCCCCAGTC		60										
AAGCCGGGGG	AATAATGAGG	TGGTGGGCGG	AACGGATTCC	AGC	ATG	GAC	GTC	TTC		115							
					Met	Asp	Val	Phe									
									1								
CAC	CTG	GAG	GGC	ATG	ACT	ACA	TCT	GTC	ATG	GCC	CAG	TTC	AAT	CTG	CTG		163
His	Leu	Glu	Gly	Met	Thr	Thr	Ser	Val	Met	Ala	Gln	Phe	Asn	Leu	Leu		
	5				10					15					20		
AGC	AGC	ACC	ATG	GAC	CAG	ATG	AGC	AGC	CGC	GCG	GCC	TCG	GCC	AGC	CCC		211
Ser	Ser	Thr	Met	Asp	Gln	Met	Ser	Ser	Arg	Ala	Ala	Ser	Ala	Ser	Pro		
				25					30					35			
TAC	ACC	CCA	GAG	CAC	GCC	GCC	AGC	GTG	CCC	ACC	CAC	TCG	CCC	TAC	GCA		259
Tyr	Thr	Pro	Glu	His	Ala	Ala	Ser	Val	Pro	Thr	His	Ser	Pro	Tyr	Ala		
			40					45					50				
CAA	CCC	AGC	TCC	ACC	TTC	GAC	ACC	ATG	TCG	CCG	GCG	CCT	GTC	ATC	CCC		307
Gln	Pro	Ser	Ser	Thr	Phe	Asp	Thr	Met	Ser	Pro	Ala	Pro	Val	Ile	Pro		
			55				60					65					
TCC	AAC	ACC	GAC	TAC	CCC	GGA	GCC	CAC	CAC	TTT	GAG	GTC	ACT	TTC	CAG		355
Ser	Asn	Thr	Asp	Tyr	Pro	Gly	Pro	His	His	Phe	Glu	Val	Thr	Phe	Gln		
	70					75					80						
CAG	TCC	AGC	ACG	GCC	AAG	TCA	GCC	ACC	TGG	ACG	TAC	TCC	CCG	CTC	TTG		403
Gln	Ser	Ser	Thr	Ala	Lys	Ser	Ala	Thr	Trp	Thr	Tyr	Ser	Pro	Leu	Leu		
	85				90					95					100		
AAG	AAA	CTC	TAC	TGC	CAG	ATC	GCC	AAG	ACA	TGC	CCC	ATC	CAG	ATC	AAG		451
Lys	Lys	Leu	Tyr	Cys	Gln	Ile	Ala	Lys	Thr	Cys	Pro	Ile	Gln	Ile	Lys		
				105				110						115			
GTG	TCC	ACC	CCG	CCA	CCC	CCA	GGC	ACT	GCC	ATC	CGG	GCC	ATG	CCT	GTT		499
Val	Ser	Thr	Pro	Pro	Pro	Pro	Gly	Thr	Ala	Ile	Arg	Ala	Met	Pro	Val		
			120					125					130				
TAC	AAG	AAA	GCG	GAG	CAC	GTG	ACC	GAC	GTC	GTG	AAA	CGC	TGC	CCC	AAC		547
Tyr	Lys	Lys	Ala	Glu	His	Val	Thr	Asp	Val	Val	Lys	Arg	Cys	Pro	Asn		
		135					140					145					
CAC	GAG	CTC	GGG	AGG	GAC	TTC	AAC	GAA	GGA	CAG	TCT	GCT	CCA	GCC	AGC		595
His	Glu	Leu	Gly	Arg	Asp	Phe	Asn	Glu	Gly	Gln	Ser	Ala	Pro	Ala	Ser		
	150					155					160						
CAC	CTC	ATC	CGC	GTG	GAA	GGC	AAT	AAT	CTC	TCG	CAG	TAT	GTG	GAT	GAC		643
His	Leu	Ile	Arg	Val	Glu	Gly	Asn	Asn	Leu	Ser	Gln	Tyr	Val	Asp	Asp		
	165				170					175					180		
CCT	GTC	ACC	GGC	AGG	CAG	AGC	GTC	GTG	GTG	CCC	TAT	GAG	CCA	CCA	CAG		691
Pro	Val	Thr	Gly	Arg	Gln	Ser	Val	Val	Val	Pro	Tyr	Glu	Pro	Pro	Gln		
				185					1								

883

Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp His  
 245 250 255 260  
 TAC CGG GAG CAG CAG GCC CTG AAC GAG AGC TCC GCC AAG AAC GGG GCC 931  
 Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala Lys Asn Gly Ala  
 265 270 275  
 GCC AGC AAG CGT GCC TTC AAG CAG AGC CCC CCT GCC GTC CCC GCC CTT 979  
 Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala Val Pro Ala Leu  
 280 285 290  
 GGT GCC GGT GTG AAG AAG CGG CGG CAT GGA GAC GAG GAC ACG TAC TAC 1027  
 Gly Ala Gly Val Lys Lys Arg Arg His Gly Asp Glu Asp Thr Tyr Tyr  
 295 300 305  
 CTT CAG GTG CGA GGC CGG GAG AAC TTT GAG ATC CTG ATG AAG CTG AAA 1075  
 Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu Met Lys Leu Lys  
 310 315 320  
 GAG AGC CTG GAG CTG ATG GAG TTG GTG CCG CAG CCA CTG GTG GAC TCC 1123  
 Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro Leu Val Asp Ser  
 325 330 335 340  
 TAT CGG CAG CAG CAG CAG CTC CTA CAG AGG CCG AGT CAC CTA CAG CCC 1171  
 Tyr Arg Gln Gln Gln Gln Leu Leu Gln Arg Pro Ser His Leu Gln Pro  
 345 350 355  
 CCG TCC TAC GGG CCG GTC CTC TCG CCC ATG AAC AAG GTG CAC GGG GGC 1219  
 Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys Val His Gly Gly  
 360 365 370  
 ATG AAC AAG CTG CCC TCC GTC AAC CAG CTG GTG GGC CAG CCT CCC CCG 1267  
 Met Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly Gln Pro Pro Pro  
 375 380 385  
 CAC AGT TCG GCA GCT ACA CCC AAC CTG GGG CCC GTG GGC CCC GGG ATG 1315  
 His Ser Ser Ala Ala Thr Pro Asn Leu Gly Pro Val Gly Pro Gly Met  
 390 395 400  
 CTC AAC AAC CAT GGC CAC GCA GTG CCA GCC AAC GGC GAG ATG AGC AGC 1363  
 Leu Asn Asn His Gly His Ala Val Pro Ala Asn Gly Glu Met Ser Ser  
 405 410 415 420  
 AGC CAC AGC GCC CAG TCC ATG GTC TCG GGG TCC CAC TCC ACT CCG CCA 1411  
 Ser His Ser Ala Gln Ser Met Val Ser Gly Ser His Cys Thr Pro Pro  
 425 430 435  
 CCC CCC TAC CAC GCC GAC CCC AGC CTC GTC AGT TTT TTA ACG GGA TTG 1459  
 Pro Pro Tyr His Ala Asp Pro Ser Leu Val Ser Phe Leu Thr Gly Leu  
 440 445 450  
 GGG TGT CCA AAC TGC ATC GAG TAT TTC ACC TCC CAA GGG TTA CAG AGC 1507  
 Gly Cys Pro Asn Cys Ile Glu Tyr Phe Thr Ser Gln Gly Leu Gln Ser  
 455 460 465  
 ATT TAC CAC CTG CAG AAC CTG ACC ATT GAG GAC CTG GGG GCC CTG AAG 1555  
 Ile Tyr His Leu Gln Asn Leu Thr Ile Glu Asp Leu Gly Ala Leu Lys  
 470 475 480  
 ATC CCC GAG CAG TAC CGC ATG ACC ATC TGG CGG GGC CTG CAG GAC CTG 1603  
 Ile Pro Glu Gln Tyr Arg Met Thr Ile Trp Arg Gly Leu Gln Asp Leu  
 485 490 495 500  
 AAG CAG GGC CAC GAC TAC AGC ACC GCG CAG CAG CTG CTC CGC TCT AGC 1651  
 Lys Gln Gly His Asp Tyr Ser Thr Ala Gln Gln Leu Leu Arg Ser Ser  
 505 510 515  
 AAC GCG GCC ACC ATC TCC ATC GGC GGC TCA GGG GAA CTG CAG CGC CAG 1699  
 Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu Leu Gln Arg Gln  
 520 525 530  
 CGG GTC ATG GAG GCC GTG CAC TTC CGC GTG CGC CAC ACC ATC ACC ATC 1747

Ile Ile Ile Thr Leu Glu Met Arg Asp Gly Gln Val Leu Gly Arg Arg  
225 230 235 240

Ans  
AS  
Wk

Ser Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala  
 245 250 255  
 Asp Glu Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala  
 260 265 270  
 Lys Asn Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala  
 275 280 285  
 Val Pro Ala Leu Gly Ala Gly Val Lys Lys Arg Arg His Gly Asp Glu  
 290 295 300  
 Asp Thr Tyr Tyr Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu  
 305 310 315 320  
 Met Lys Leu Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro  
 325 330 335  
 Leu Val Asp Ser Tyr Arg Gln Gln Gln Gln Leu Leu Gln Arg Pro Ser  
 340 345 350  
 His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys  
 355 360 365  
 Val His Gly Gly Met Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly  
 370 375 380  
 Gln Pro Pro Pro His Ser Ser Ala Ala Thr Pro Asn Leu Gly Pro Val  
 385 390 395 400  
 Gly Pro Gly Met Leu Asn Asn His Gly His Ala Val Pro Ala Asn Gly  
 405 410 415  
 Glu Met Ser Ser Ser His Ser Ala Gln Ser Met Val Ser Gly Ser His  
 420 425 430  
 Cys Thr Pro Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Ser Phe  
 435 440 445  
 Leu Thr Gly Leu Gly Cys Pro Asn Cys Ile Glu Tyr Phe Thr Ser Gln  
 450 455 460  
 Gly Leu Gln Ser Ile Tyr His Leu Gln Asn Leu Thr Ile Glu Asp Leu  
 465 470 475 480  
 Gly Ala Leu Lys Ile Pro Glu Gln Tyr Arg Met Thr Ile Trp Arg Gly  
 485 490 495  
 Leu Gln Asp Leu Lys Gln Gly His Asp Tyr Ser Thr Ala Gln Gln Leu  
 500 505 510  
 Leu Arg Ser Ser Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu  
 515 520 525  
 Leu Gln Arg Gln Arg Val Met Glu Ala Val His Phe Arg Val Arg His  
 530 535 540  
 Thr Ile Thr Ile Pro Asn Arg Gly Gly Pro Gly Gly Gly Pro Asp Glu  
 545 550 555 560  
 Trp Ala Asp Phe Gly Phe Asp Leu Pro Asp Cys Lys Ala Arg Lys Gln  
 565 570 575  
 Pro Ile Lys Glu Glu Phe Thr Glu Ala Glu Ile His  
 580 585

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1817 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

ATGGCCAGT CCACCGCTAC CTCCCCTGAT GGGGGCACCA CGTTTGAGCA CCTCTGGAGC 60  
 TCTCTGGAAC CAGACAGCAC CTACTTCGAC CTTCCCCAGT CAAGCCGGGG GAATAATGAG 120  
 GTGGTGGGCG GAACGGATTG CAGCATGGAC GTCTTCACCC TGGAGGGCAT GACTACATCT 180  
 GTCATGGCCC AGTTCAATCT GTTGAGCAGC ACCATGGACC AGATGAGCAG CCGCGCGGCC 240  
 TCGGCCAGCC CCTACACCCC AGAGCACGCC GCCAGCGTGC CCACCCACTC GCCCTACGCA 300  
 CAACCCAGCT CCACCTTCGA CACCATGTCT CCGGCGCCTG TCATCCCCCTC CAACACCGAC 360  
 TACCCCGGAC CCCACCACTT TGAGGTCACT TTCCAGCAGT CCAGCACGGC CAAGTCAGCC 420  
 ACCTGGACGT ACTCCCCGCT CTTGAAGAAA CTCTACTGCC AGATCGCCAA GACATGCCCC 480  
 ATCCAGATCA AGGTGTCCAC CCCGCCACCC CCAGGCACTG CCATCCGGGC CATGCCTGTT 540  
 TACAAGAAAG CGGAGCACGT GACCGACGTC GTGAAACGCT GCCCCAACCA CGAGCTCGGG 600  
 AGGGACTTCA ACGAAGGACA GTCTGCTCCA GCCAGCCACC TCATCCGCGT GGAAGGCAAT 660  
 AATCTCTCGC AGTATGTGGA TGACCCTGTC ACCCGCAGGC AGAGCGTCGT GGTGCCCTAT 720  
 GAGCCACCAC AGGTGGGGAC GGAATTCACC ACCATCTGT ACAACTTCAT GTGTAACAGC 780  
 AGCTGTGTAG GGGGCATGAA CCGGCGGCCC ATCCTCATCA TCATCACCCT GGAGATGCGG 840  
 GATGGGCAGG TGCTGGGCGG CCGGTCCTTT GAGGGCCGCA TCTGCGCCTG TCCTGGCCGC 900  
 GACCGAAAAG CTGATGAGGA CCACTACCGG GAGCAGCAGG CCCTGAACGA GAGCTCCGCC 960  
 AAGAACGGGG CCGCCAGCAA GCGTGCCTTC AAGCAGAGCC CCGCTGCCGT CCCC GCCCTT 1020  
 GGTGCCGGTG TGAAGAAGCG GCGGCATGGA GACGAGGACA CGTACTACCT TCAGGTGCGA 1080  
 GGCCGGGAGA ACTTTGAGAT CCTGATGAAG CTGAAAGAGA GCCTGGAGCT GATGGAGTTG 1140  
 GTGCCGCAGC CACTGGTGGA CTCCTATCGG CAGCAGCAGC AGCTCCTACA GAGGCCGAGT 1200  
 CACCTACAGC CCCCCTCCTA CCGGCGGCTC CTCTCGCCCA TGAACAAGGT GCACGGGGGC 1260  
 ATGAACAAGC TGCCCTCCGT CAACCAGCTG GTGGGCCAGC CTCCCCCGCA CAGTTCGGCA 1320  
 GCTACACCCA ACCTGGGGCC CGTGGGCCCC GGGATGCTCA ACAACCATGG CCACGCAGTG 1380  
 CCAGCCAACG GCGAGATGAG CAGCAGCCAC AGCGCCAGT CCATGGTCTC GGGGTCCAC 1440  
 TGCACTCCGC CACCCCCCTA CCACGCCGAC CCCAGCCTCG TCAGGACCTG GGGGCCCTGA 1500  
 AGATCCCCGA GCAGTACCGC ATGACCATCT GGCGGGGCCT GCAGGACCTG AAGCAGGACC 1560  
 ACGACTACAG CACCGCGCAG CAGCTGCTCC GCTCTAGCAA CGCGGCCACC ATCTCCATCG 1620  
 GCGGCTCAGG GGAAGTGCAG CGCCAGCGGG TCATGGAGGC CGTGCACTTC CGCGTGCGCC 1680  
 ACACCATCAC CATCCCCAAC CGCGGCGGCC CAGGCGGGCG CCCTGACGAG TGGGCGGACT 1740  
 TCGGCTTCGA CCTGCCCCGAC TGCAAGGCCC GCAAGCAGCC CATCAAGGAG GAGTTCACGG 1800  
 AGGCCGAGAT CCACTGA 1817

mb  
AS

(A) LENGTH: 499 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(21) MOLECULE TYPE: protein

Met Ala Gln Ser Thr Ala Thr Ser Pro Asp Gly Gly Thr Thr Phe Glu  
1 5 10 15  
His Leu Trp Ser Ser Leu Glu Pro Asp Ser Thr Tyr Phe Asp Leu Pro  
20 25 30  
Gln Ser Ser Arg Gly Asn Asn Glu Val Val Gly Gly Thr Asp Ser Ser  
35 40 45  
Met Asp Val Phe His Leu Glu Gly Met Thr Thr Ser Val Met Ala Gln  
50 55 60  
Phe Asn Leu Leu Ser Ser Thr Met Asp Gln Met Ser Ser Arg Ala Ala  
65 70 75 80  
Ser Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His  
85 90 95  
Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala  
100 105 110  
Pro Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu  
115 120 125  
Val Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr  
130 135 140  
Ser Pro Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro  
145 150 155 160  
Ile Gln Ile Lys Val Ser Thr Pro Pro Pro Gly Thr Ala Ile Arg  
165 170 175  
Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Val Val Lys  
180 185 190  
Arg Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser  
195 200 205  
Ala Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln  
210 215 220  
Tyr Val Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr  
225 230 235 240  
Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe  
245 250 255  
Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu  
260 265 270  
Ile Ile Ile Thr Leu Glu Met Arg Asp Gly Gln Val Leu Gly Arg Arg  
275 280 285  
Ser Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala  
290 295 300  
Asp Glu Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala  
305 310 315 320



*[Handwritten signature]*

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 17 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

17

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GGTTCTGCGAG GTGACTCAG

19

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

GCCATGCCTG TCTACAAG

18

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ACCAGCTGGT TGACGGAG

18

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GTCAACCAGC TGGTGGGCCA G

21

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

GTGGATCTCG GCCTCC

16

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

AGGCCGGCGT GGGGAAG

17

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

CTTGGCGATC TGGCAGTAG

19

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

GCGGCCACGA CCGTGAC

17

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

seq 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

Sub  
A5  
Cat

GGCAGCTTGG GTCTCTGG

18

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

CTGTACGTCG GTGACCCC

18

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

TCAGTGGATC TCGGCCTC

18

(2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

AGGGGACGCA GCGAAACC

18

(2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CCATCAGCTC CAGGCTCTC

19

(2) INFORMATION FOR SEQ ID NO: 34:

- (1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

CCAGGACAGG CGCAGATG

18

(2) INFORMATION FOR SEQ ID NO: 35:

- (1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GATGAGGTGG CTGGCTGGA

19

(2) INFORMATION FOR SEQ ID NO: 36:

- (1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

TGGTCAGGTT CTGCAGGTG

19

(2) INFORMATION FOR SEQ ID NO: 37:

- (1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

CACCTACTCC AGGGATGC

18

(2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

AGGAAAATAG AAGCGTCAGT C

21

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CAGGCCCACT TGCCTGCC

18

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

CTGTCCCCAA GCTGATGAG

19